What is claimed:

1. A method of profiling mRNA production during stages comprising:

isolating a plurality of cells each characterized by a different stage of disease progression;

antisense RNA transcripts from mRNA of each of the plurality of cells;

amplifying the antisense RNA transcripts; and

quantitating the levels of individual antisense RNA transcripts which is indicative of levels of an mRNA for each of the plurality of cells.

2. The method according to claim 1, wherein isolation of the cells comprises enzymatic treatment of the cells.

3. The method according to claim 1, wherein isolation of the cells comprises laser separation of the cells.

4. The method according to claim 1, wherein isolation of the cells comprises floating the cells out of a sample.

5. The method according to claim 1, wherein the disease is Alzheimer's disease.

6. The method according to claim 5, wherein the plurality of cells are neurofibrillary tangle cells.

7. The method according to claim 5, wherein the RNA transcripts are encoded by a gene selected from the group consisting of (1)synaptic markers, (2) lysosomal hydrolases, (3) kinases and phosphatases, (4) neurotrophic factors, (5) cell cycle regulators, (6) apoptosis factors, (7) mitochondrial genes, and (8) other proteins associated with Alzheimer's disease.

8. The method according to claim 1, wherein the quantitating of the antisense RNA transcripts is carried out by dot-blot hybridization of cDNA with the antisense RNA transcripts.

9. The method according to claim 1, wherein the quantitating of the antisense RNA transcripts is carried out by sequencing based serial analysis of gene expression.

10. The method according to claim 1, wherein the quantitating of the antisense RNA transcripts is carried out by cDNA microarray analysis.

11. The method according to claim 1, wherein the cells are isolated from brain tissue.

12. The method according to claim 1, wherein the isolating a plurality of cells is carried out from a post mortem sample of cells.

13. The method according to claim 1, wherein the isolating a plurality of cells is carried out from a sample collected from a living patient.

14. The method according to claim 13, wherein the sample is selected from the group consisting of blood, cheek scrapings, cerebral spinal fluid, saliva, urine, and skin.

15. The method according to claim 1, further comprising:

measuring mRNA levels for control genes by quantitating the levels of antisense RNA transcripts for the control genes; and

comparing the mRNA levels for the transcripts to the mRNA levels for the control gene transcripts using multivariate analysis.

16. A method for monitoring gene expression in a single cell, comprising:

isolating a cell from tissue;

producing antisense RNA transcripts from mRNA of the cell;

amplifying the antisense RNA transcripts; and

measuring mRNA levels for individual genes within the cell by quantitating the levels of the antisense RNA transcripts.

17. The method according to claim 16, further comprising:

producing antisense RNA transcripts from mRNA of a second cell;

amplifying the antisense RNA transcripts from the second cell;

measuring mRNA levels for individual genes within the second cell by quantitating the levels of the antisense RNA transcripts; and

comparing the mRNA level for a gene expressed in the cell as determined according to the method of claim 16 to the mRNA level for the gene expressed in the second cell.

18. The method according to claim 16, wherein isolation of the cells comprises enzymatic treatment of the tissue.

19. The method according to claim 16, wherein isolation of the cells comprises laser separation of the cell from the tissue.

20. The method according to claim 16, wherein isolation of the cells comprises floating the cells out of a sample.

21. The method according to claim 16, wherein the quantitating of the antisense RNA transcripts is carried out by dot-blot hybridization of cDNA with the antisense RNA transcripts.

22. The method according to claim 16, wherein the quantitating of the antisense RNA transcripts is carried out by sequencing based serial analysis of gene expression.

23. The method according to claim 16, wherein the quantitating of the antisense RNA transcripts is carried out by cDNA microarray analysis.

24. The method according to claim 16, wherein the cells are isolated from brain tissue.

25. The method according to claim 16, wherein the isolating a plurality of cells is carried out from a post mortem sample of cells.

26. The method according to claim 16, wherein the isolating a plurality of cells is carried out from a sample collected from a living patient.

27. The method according to claim 26, wherein the sample is selected from the group consisting of blood, cheek scrapings, cerebral spinal fluid, saliva, urine, and skin.

28. The method according to claim 16, further comprising:

measuring mRNA levels for control genes by quantitating the levels of antisense RNA transcripts for control genes; and

comparing the mRNA levels for the transcripts to the mRNA levels for the control gene transcripts using multivariate analysis.

29. The method according to claim 17, wherein the first and second cells are at different stages of development.

30. The method according to claim 17, wherein the first cell is diseased and the second cell is healthy.

31. The method according to claim 30, wherein the disease is Alzheimer's disease.

32. The method according to claim 31, wherein the cell is a neurofibrillary tangle cell.

33. The method according to claim 31, wherein the RNA transcripts are encoded by a gene selected from the group consisting of (1)synaptic markers, (2) lysosomal hydrolases, (3) kinases and phosphatases, (4) neurotrophic factors, (5) cell

cycle regulators, (6) apoptosis factors, (7) mitochondrial genes, and (8) other proteins associated with Alzheimer's disease.

34. The method according to claim 17, wherein the first cell is exposed to an experimental compound and the second cell is exposed to a different or no compound.

35. The method according to claim 34, wherein the compound is an experimental drug.

36. The method according to claim 34, wherein the compound is an environmental toxin

37. The method according to claim 16, wherein the first cell is exposed to an environmental stimulus and the second cell is not exposed to the environmental stimulus.

38. The method according to claim 37, wherein the environmental stimulus is a form of radiation.

39. A method of diagnosing or monitoring progression of a disease comprising:

classifying cells as diseased or healthy;

isolating a single cell which is classified as diseased from a subject;

producing antisense RNA transcripts from mRNA of the isolated cell:

amplifying the antisense RNA transcripts; and

measuring mRNA levels for quantification of the RNA transcripts.

40. The method according to claim 39, wherein the isolating of the cells comprises enzymatic treatment of the tissue.

41. The method according to claim 39, wherein the isolating of the cells comprises laser separation of the cell from the tissue.

42. The method according to claim 39, wherein the isolating of the cells comprises floating the cells out of a sample.

43. The method according to claim 39, wherein the quantification of the antisense RNA transcripts is carried out by dot-blot hybridization of cDNA with the antisense RNA transcripts.

44. The method according to claim 39, wherein the quantification of the antisense RNA transcripts is carried out by sequencing based serial analysis of gene expression.

45. The method according to claim 39, wherein the quantification of the antisense RNA transcripts is carried out by cDNA microarray analysis.

46. The method according to claim 39, wherein the cells are isolated from brain tissue.

47. The method according to claim 39, wherein the isolating is carried out from a post mortem sample of cells.

48. The method according to claim 39, wherein the isolating is carried out from a sample collected from a living patient.

49. The method according to claim 48, wherein the sample is selected from the group consisting of blood, cheek scrapings, cerebral spinal fluid, saliva, urine, and skin.

50. The method according to claim 39, further comprising:

measuring mRNA levels for control genes by quantitating the levels of antisense RNA transcripts for control genes; and

comparing the mRNA levels for the transcripts to the mRNA levels for the control gene transcripts using multivariate analysis.

51. The method according to claim 39, wherein the disease is Alzheimer's disease.

52. The method according to claim 51, wherein the cells are neurofibrillary tangle cells.

53. The method according to claim 51, wherein the RNA transcripts are encoded by a gene selected from the group consisting of (1)synaptic markers, (2) lysosomal hydrolases, (3) kinases and phosphatases, (4) neurotrophic factors, (5) cell cycle regulators, (6) apoptosis factors, (7) mitochondrial genes, and (8) other proteins associated with Alzheimer's disease.

54. The method according to claim 39, wherein said classifying cells as diseased or healthy is carried out by sorting cells on the basis of morphology.

55. The method according to claim 39, wherein said classifying cells as diseased or healthy is carried out by sorting cells on the basis of size.

56. The method according to claim 39, wherein said classifying cells as diseased or healthy is carried out by sorting cells on the basis of immunological markers.